CRF Errors Corrected by th STIC Syst ms Branch

Serial Number: 08/785,455

CRF Processing Date: 2/21/99
Edited by: _____
Verified by: _____ (STIC staff)

ENTERED #2

☐ Changed a fil from non-ASCII to ASCII

☐ Changed the margins in cases wh re the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number input ed by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integ r.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☑ Deleted extra, invalid, headings used by an applicant, specifically:
"APPLICANT"

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: added (B) FILING DATE; heading under (vi) CURRENT APPLICATION DATA;

_____

_____

*Examin r: Th abov corrections must b communicated to the applicant in the first Offic Action. DO NOT s nd a copy of this form.

3/1/95

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)     General Information
 4
 5              (i) APPLICANT
 6                  (A) NAME:  Hodgson, John
 7                  (B) STREET: Great West Road
 8                  (C) CITY: Brentford
 9                  (D) STATE OR PROVINCE: Middlesex
10                  (E) COUNTRY: United Kingdom
11                  (F) POSTAL CODE: TW8 9EP
12
13    APPLICANT
14                  (A) NAME:  Hodgson, John
15                  (B) STREET: Great West Road
16                  (C) CITY: Brentford
17                  (D) STATE OR PROVINCE: Middlesex
18                  (E) COUNTRY: United Kingdom
19                  (F) POSTAL CODE: TW8 9EP
20
21              (ii) TITLE OF THE INVENTION: Novel tRNA Synthetase
22
23
24              (iii) NUMBER OF SEQUENCES: 2
25
26              (iv) COMPUTER-READABLE FORM:
27                  (A) MEDIUM TYPE: Diskette
28                  (B) COMPUTER: IBM Compatible
29                  (C) OPERATING SYSTEM: DOS
30                  (D) SOFTWARE: FastSEQ for Windows Version 2.0
31
32              (v) CURRENT APPLICATION DATA:
33                  (A) APPLICATION NUMBER:
34                  (B) FILING DATE:
35                  (2) INFORMATION FOR SEQ ID NO:1:
36
37              (i) SEQUENCE CHARACTERISTICS:
38                  (A) LENGTH: 1974 base pairs
39                  (B) TYPE: nucleic acid
40                  (C) STRANDEDNESS: double
41                  (D) TOPOLOGY: linear
42
43              (ii) MOLECULE TYPE: Genomic DNA
44
45              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
46
```

Lines with `-->` markers: 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 17, 18, 19

```
47   ATGGCTAAAG AAACATTTTA TATAACAACC CCAATATACT ATCCTAGTGG GAATTTACAT     60
48   ATAGGACATG CATATTCTAC AGTGGCTGGA GATGTTATTG CAAGATATAA GAGAATGCAA    120
49   GGATATGATG TTCGTTATTT GACTGGAACG GATGAACACG GTCAAAAAAT TCAAGAAAAA    180
50   GCTCAAAAAG CTGGTAAGAC AGAAATTGAA TATTTGGATG AGATGATTGC TGGAATTAAA    240
51   CAATTGTGGG CTAAGCTTGA AATTTCAAAT GATGATTTTA TCAGAACAAC TGAAGAACGT    300
52   CATAAACATG TCGTTGAGCA AGTGTTTGAA CGTTTATTAA AGCAAGGTGA TATCTATTTA    360
53   GGTGAATATG AAGGTTGGTA TTCTGTTCCG GATGAAACAT ACTATACAGA GTCACAATTA    420
54   GTAGACCCAC AATACGAAAA CGGTAAAATT ATTGGTGGCA AAAGTCCAGA TTCTGGACAC    480
55   GAAGTTGAAC TAGTTAAAGA AGAAAGTTAT TTCTTTAATA TTAGTAAATA TACAGACCGT    540
56   TTATTAGAGT TCTATGACCA AAATCCAGAT TTTATACAAC CACCATCAAG AAAAAATGAA    600
57   ATGATTAACA ACTTCATTAA ACCAGGACTT GCTGATTTAG CTGTTTCTCG TACATCATTT    660
58   AACTGGGGTG TCCATGTTCC GTCTAATCCA AAACATGTTG TTTATGTTTG GATTGATGCG    720
59   TTAGTTAACT ATATTTCAGC ATTAGGCTAT TTATCAGATG ATGAGTCACT ATTTAACAAA    780
60   TACTGGCCAG CAGATATTCA TTTAATGGCT AAGGAAATTG TGCGATTCCA CTCAATTATT    840
61   TGGCCTATTT TATTGATGGC ATTAGACTTA CCGTTACCTA AAAAAGTCTT TGCACATGGT    900
62   TGGATTTTGA TGAAAGATGG AAAAATGAGT AAATCTAAAG GTAATGTTGT AGACCCTAAT    960
63   ATTTTAATTG ATCGCTATGG TTTAGATGCT ACACGTTATT ATCTAATGCG TGAATTACCA   1020
64   TTTGGTTCAG ATGGCGTATT TACACCTGAA GCATTGTTG AGCGTACAAA TTTCGATCTA   1080
65   GCAAATGACT TAGGTAACTT AGTAAACCGT ACGATTTCTA TGGTTAATAA GTACTTTGAT   1140
66   GGCGAATTAC CAGCGTATCA AGGTCCACTT CATGAATTAG ATGAAGAAAT GGAAGCTATG   1200
67   GCTTTAGAAA CAGTGAAAAG CTACACTGAA AGCATGGAAA GTTTGCAATT TTCTGTGGCA   1260
68   TTATCTACGG TATGGAAGTT TATAAGTAGA ACGAATAAGT ATATTGACGA AACAACGCCT   1320
69   TGGGTATTAG CTAAGGACGA TAGCCAAAAA GATATGTTAG GCAATGTAAT GGCTCACTTA   1380
70   GTTGAAAATA TTCGTTATGC AGCTGTATTA TTACGTCCAT TCTTAACACA TGCGCCGAAA   1440
71   GAGATTTTTG AACAATTGAA CATAAACAAT CCTCAATTTA TGGAATTTAG TAGTTTAGAG   1500
72   CAATATGGTG TGCTTACTGA GTCAATTATG GTTACTGGGC AACCTAAACC TATTTTCCCA   1560
73   AGATTGGATA GCGAAGCGGA AATTGCATAT ATCAAAGAAT CAATGCAACC GCCTGCTACT   1620
74   GAAGAGGAAA AAGAAGAGAT TCCTAGCAAA CCTCAAATTG ATATTAAAGA CTTTGATAAA   1680
75   GTTGAAATTA AGGCAGCAAC GATTATTGAT GCTGAACATG TTAAGAAGTC AGATAAGCTT   1740
76   TTAAAAATTC AAGTAGACTT AGATTCTGAA CAAAGACAAA TTGTATCAGG AATTGCCAAA   1800
77   TTCTATACAC CAGATGATAT TATTGGTAAA AAAGTAGCAG TTGTTACTAA CCTGAAACCA   1860
78   GCTAAATTAA TGGGACAAAA ATCTGAAGGT ATGATATTAT CTGCTGAAAA AGATGGTGTA   1920
79   TTAACCTTAG TAAGTTTACC AAGTGCAATT CCAAATGGTG CAGTGATTAA ATAA         1974
80
81           (2) INFORMATION FOR SEQ ID NO:2:
82
83        (i) SEQUENCE CHARACTERISTICS:
84           (A) LENGTH: 657 amino acids
85           (B) TYPE: amino acid
86           (C) STRANDEDNESS: single
87           (D) TOPOLOGY: linear
88
89        (ii) MOLECULE TYPE: peptide
90
91        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
92
93   Met Ala Lys Glu Thr Phe Tyr Ile Thr Thr Pro Ile Tyr Tyr Pro Ser
94    1               5                  10                  15
95   Gly Asn Leu His Ile Gly His Ala Tyr Ser Thr Val Ala Gly Asp Val
96                20                  25                  30
97   Ile Ala Arg Tyr Lys Arg Met Gln Gly Tyr Asp Val Arg Tyr Leu Thr
98            35                  40                  45
99   Gly Thr Asp Glu His Gly Gln Lys Ile Gln Glu Lys Ala Gln Lys Ala
```

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100        50                    55                    60
101    Gly Lys Thr Glu Ile Glu Tyr Leu Asp Glu Met Ile Ala Gly Ile Lys
102    65                    70                    75                    80
103    Gln Leu Trp Ala Lys Leu Glu Ile Ser Asn Asp Asp Phe Ile Arg Thr
104                        85                    90                    95
105    Thr Glu Glu Arg His Lys His Val Val Glu Gln Val Phe Glu Arg Leu
106                    100                   105                   110
107    Leu Lys Gln Gly Asp Ile Tyr Leu Gly Glu Tyr Glu Gly Trp Tyr Ser
108                    115                   120                   125
109    Val Pro Asp Glu Thr Tyr Tyr Thr Glu Ser Gln Leu Val Asp Pro Gln
110                    130                   135                   140
111    Tyr Glu Asn Gly Lys Ile Ile Gly Gly Lys Ser Pro Asp Ser Gly His
112    145                   150                   155                   160
113    Glu Val Glu Leu Val Lys Glu Glu Ser Tyr Phe Phe Asn Ile Ser Lys
114                    165                   170                   175
115    Tyr Thr Asp Arg Leu Leu Glu Phe Tyr Asp Gln Asn Pro Asp Phe Ile
116                    180                   185                   190
117    Gln Pro Pro Ser Arg Lys Asn Glu Met Ile Asn Asn Phe Ile Lys Pro
118                    195                   200                   205
119    Gly Leu Ala Asp Leu Ala Val Ser Arg Thr Ser Phe Asn Trp Gly Val
120                    210                   215                   220
121    His Val Pro Ser Asn Pro Lys His Val Val Tyr Val Trp Ile Asp Ala
122    225                   230                   235                   240
123    Leu Val Asn Tyr Ile Ser Ala Leu Gly Tyr Leu Ser Asp Asp Glu Ser
124                    245                   250                   255
125    Leu Phe Asn Lys Tyr Trp Pro Ala Asp Ile His Leu Met Ala Lys Glu
126                    260                   265                   270
127    Ile Val Arg Phe His Ser Ile Ile Trp Pro Ile Leu Leu Met Ala Leu
128                    275                   280                   285
129    Asp Leu Pro Leu Pro Lys Lys Val Phe Ala His Gly Trp Ile Leu Met
130                    290                   295                   300
131    Lys Asp Gly Lys Met Ser Lys Ser Lys Gly Asn Val Val Asp Pro Asn
132    305                   310                   315                   320
133    Ile Leu Ile Asp Arg Tyr Gly Leu Asp Ala Thr Arg Tyr Tyr Leu Met
134                    325                   330                   335
135    Arg Glu Leu Pro Phe Gly Ser Asp Gly Val Phe Thr Pro Glu Ala Phe
136                    340                   345                   350
137    Val Glu Arg Thr Asn Phe Asp Leu Ala Asn Asp Leu Gly Asn Leu Val
138                    355                   360                   365
139    Asn Arg Thr Ile Ser Met Val Asn Lys Tyr Phe Asp Gly Glu Leu Pro
140                    370                   375                   380
141    Ala Tyr Gln Gly Pro Leu His Glu Leu Asp Glu Glu Met Glu Ala Met
142    385                   390                   395                   400
143    Ala Leu Glu Thr Val Lys Ser Tyr Thr Glu Ser Met Glu Ser Leu Gln
144                    405                   410                   415
145    Phe Ser Val Ala Leu Ser Thr Val Trp Lys Phe Ile Ser Arg Thr Asn
146                    420                   425                   430
147    Lys Tyr Ile Asp Glu Thr Thr Pro Trp Val Leu Ala Lys Asp Asp Ser
148                    435                   440                   445
149    Gln Lys Asp Met Leu Gly Asn Val Met Ala His Leu Val Glu Asn Ile
150                    450                   455                   460
151    Arg Tyr Ala Ala Val Leu Leu Arg Pro Phe Leu Thr His Ala Pro Lys
152    465                   470                   475                   480
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153	Glu	Ile	Phe	Glu	Gln	Leu	Asn	Ile	Asn	Asn	Pro	Gln	Ph	Met	Glu	Phe
154				485					490					495		
155	Ser	Ser	Leu	Glu	Gln	Tyr	Gly	Val	Leu	Thr	Glu	Ser	Ile	Met	Val	Thr
156				500				505					510			
157	Gly	Gln	Pro	Lys	Pro	Ile	Phe	Pro	Arg	Leu	Asp	Ser	Glu	Ala	Glu	Ile
158			515					520				525				
159	Ala	Tyr	Ile	Lys	Glu	Ser	Met	Gln	Pro	Pro	Ala	Thr	Glu	Glu	Glu	Lys
160		530					535				540					
161	Glu	Glu	Ile	Pro	Ser	Lys	Pro	Gln	Ile	Asp	Ile	Lys	Asp	Phe	Asp	Lys
162	545				550				555							560
163	Val	Glu	Ile	Lys	Ala	Ala	Thr	Ile	Ile	Asp	Ala	Glu	His	Val	Lys	Lys
164				565				570					575			
165	Ser	Asp	Lys	Leu	Leu	Lys	Ile	Gln	Val	Asp	Leu	Asp	Ser	Glu	Gln	Arg
166				580				585					590			
167	Gln	Ile	Val	Ser	Gly	Ile	Ala	Lys	Phe	Tyr	Thr	Pro	Asp	Asp	Ile	Ile
168			595					600				605				
169	Gly	Lys	Lys	Val	Ala	Val	Val	Thr	Asn	Leu	Lys	Pro	Ala	Lys	Leu	Met
170		610					615				620					
171	Gly	Gln	Lys	Ser	Glu	Gly	Met	Ile	Leu	Ser	Ala	Glu	Lys	Asp	Gly	Val
172	625				630				635					640		
173	Leu	Thr	Leu	Val	Ser	Leu	Pro	Ser	Ala	Ile	Pro	Asn	Gly	Ala	Val	Ile
174				645				650				655				
175	Lys															
176																
177																